RESULT 1
LOL4_HUMAN
ID   LOL4_HUMAN   STANDARD;   PRT;   756 AA.
AC   Q96JB6; Q96DY1; Q96PC0; Q9H6T5;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Lysyl oxidase homolog 4 precursor (EC 1.4.3.-) (Lysyl oxidase-like
DE   protein 4) (Lysyl oxidase related protein C).
GN   LOXL4 OR LOXC.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Testis;
RX   MEDLINE=21316447; PubMed=11292829;
RA   Ito H., Akiyama H., Iguchi H., Iyama K., Miyamoto M., Ohsawa K.,
RA   Nakamura T.;
RT   "Molecular cloning and biological activity of a novel lysyl oxidase-
RT   related gene expressed in cartilage.";
RL   J. Biol. Chem. 276:24023-24029(2001).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21550107; PubMed=11691589;
RA   Maeki J.M., Tikkanen H., Kivirikko K.I.;
RT   "Cloning and characterization of a fifth human lysyl oxidase
RT   isoenzyme: the third member of the lysyl oxidase-related subfamily
RT   with four scavenger receptor cysteine-rich domains.";
RL   Matrix Biol. 20:493-496(2001).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Placenta;
RX   MEDLINE=21550106; PubMed=11691588;
RA   Asuncion L., Fogelgren B., Fong K.S.K., Fong S.F.T., Kim Y.,
RA   Csiszar K.;
RT   "A novel human lysyl oxidase-like gene (LOXL4) on chromosome 10q24 has
RT   an altered scavenger receptor cysteine rich domain.";
RL   Matrix Biol. 20:487-491(2001).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Eye;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [5]
RP SEQUENCE OF 492-756 FROM N.A.
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Okitani R., Ota T., Suzuki Y., Obayashi M., Nishi T., Shibahara T.,
RA Tanaka T., Nakamura Y., Isogai T., Sugano S.;
RT "NEDO human cDNA sequencing project.";
RL Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
CC -!- FUNCTION: May modulate the formation of a collagenous
CC extracellular matrix.
CC -!- COFACTOR: Copper and LTQ (By similarity).
CC -!- SUBCELLULAR LOCATION: Extracellular (Potential).
CC -!- TISSUE SPECIFICITY: Expressed in many tissues, the highest levels
CC among the tissues studied being in the skeletal muscle, testis and
CC pancreas. Expressed in cartilage.
CC -!- PTM: The lysine tyrosylquinone cross-link (LTQ) is generated by
CC condensation of the epsilon-amino group of a lysine with a
CC topaquinone produced by oxidation of tyrosine.
CC -!- SIMILARITY: Contains 4 SRCR domains.
CC -!- SIMILARITY: Belongs to the lysyl oxidase family.
CC ----------

CC ----------
DR EMBL; AF338441; AAK71934.1; -.
DR EMBL; AY036093; AAK64186.1; -.
DR EMBL; AF395336; AAL27543.1; -.
DR EMBL; BC007522; AAH07522.1; ALT_INIT.
DR EMBL; BC013153; AAH13153.1; -.
DR EMBL; AK025542; BAB15167.1; -.
DR Genew; HGNC:17171; LOXL4.
DR MIM; 607318; -.
DR InterPro; IPR001695; Lysyl_oxidase.
DR InterPro; IPR001190; Srcr_receptor.
DR Pfam; PF01186; Lysyl_oxidase; 1.
DR Pfam; PF00530; SRCR; 4.
DR PRINTS; PR00074; LYSYLOXIDASE.
DR PRINTS; PR00258; SPERACTRCPTR.
DR ProDom; PD013887; Lysyl_oxidase; 1.
DR SMART; SM00202; SR; 4.
DR PROSITE; PS00926; LYSYL_OXIDASE; FALSE_NEG.
DR PROSITE; PS00420; SRCR_1; 1.
DR PROSITE; PS50287; SRCR_2; 4.
KW Oxidoreductase; Copper; Glycoprotein; Repeat; Signal; LTQ.
FT SIGNAL 1 24 POTENTIAL.
FT CHAIN 25 756 LYSYL OXIDASE HOMOLOG 4.

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FT   DOMAIN        32     133        SRCR 1.
FT   DOMAIN       159     287        SRCR 2.
FT   DOMAIN       311     411        SRCR 3.
FT   DOMAIN       421     529        SRCR 4.
FT   DOMAIN       533     736        LYSYL-OXIDASE LIKE.
FT   METAL        611     611        COPPER (POTENTIAL).
FT   METAL        613     613        COPPER (POTENTIAL).
FT   METAL        615     615        COPPER (POTENTIAL).
FT   CROSSLNK     638     674        Lysine tyrosylquinone (Lys-Tyr)
FT                                   (By similarity).
FT   MOD_RES      674     674        TOPAQUINONE (BY SIMILARITY).
FT   CARBOHYD     198     198        N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     629     629        N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT       3       3        W -> R (IN REF. 4).
FT   CONFLICT     101     101        R -> Q (IN REF. 4).
FT   CONFLICT     405     405        D -> A (IN REF. 4).
FT   CONFLICT     493     493        S -> G (IN REF. 3).
FT   CONFLICT     539     539        A -> T (IN REF. 3).
FT   CONFLICT     542     542        V -> A (IN REF. 3).
FT   CONFLICT     703     703        Y -> H (IN REF. 3).
SQ   SEQUENCE   756 AA;  84483 MW;  13051ACADB922BBC CRC64;

  Query Match             99.9%;  Score 4174;  DB 1;  Length 756;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches  755;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MAWSPPATLFLFLLLLGQPPPSRPQSLGTTKLRLVGPESKPEEGRLEVLHQGQWGTVCDD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAWSPPATLFLFLLLLGQPPPSRPQSLGTTKLRLVGPESKPEEGRLEVLHQGQWGTVCDD 60

Qy         61 NFAIQEATVACRQLGFEAALTWAHSAKYGQGEGPIWLDNVRCVGTESSLDQCGSNGWGVS 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 NFAIQEATVACRQLGFEAALTWAHSAKYGQGEGPIWLDNVRCVGTESSLDQCGSNGWGVS 120

Qy        121 DCSHSEDVGVICHPRRHRGYLSETVSNALGPQGRRLEEVRLKPILASAKQHSPVTEGAVE 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 DCSHSEDVGVICHPRRHRGYLSETVSNALGPQGRRLEEVRLKPILASAKQHSPVTEGAVE 180

Qy        181 VKYEGHWRQVCDQGWTMNNSRVVCGMLGFPSEVPVDSHYYRKVWDLKMRDPKSRLKSLTN 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VKYEGHWRQVCDQGWTMNNSRVVCGMLGFPSEVPVDSHYYRKVWDLKMRDPKSRLKSLTN 240

Qy        241 KNSFWIHQVTCLGTEPHMANCQVQVAPARGKLRPACPGGMHAVVSCVAGPHFRPPKTKPQ 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 KNSFWIHQVTCLGTEPHMANCQVQVAPARGKLRPACPGGMHAVVSCVAGPHFRPPKTKPQ 300

Qy        301 RKGSWAEEPRVRLRSGAQVGEGRVEVLMNRQWGTVCDHRWNLISASVVCRQLGFGSAREA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 RKGSWAEEPRVRLRSGAQVGEGRVEVLMNRQWGTVCDHRWNLISASVVCRQLGFGSAREA 360

Qy        361 LFGARLGQGLGPIHLSEVRCRGYERTLSDCPALEGSQNGCQHENAAAVRCNVPNMGFQNQ 420
              |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db        361 LFGARLGQGLGPIHLSEVRCRGYERTLSDCPALEGSQNGCQHENDAAVRCNVPNMGFQNQ 420

Qy        421 VRLAGGRIPEEGLLEVQVEVNGVPRWGSVCSENWGLTEAMVACRQLGLGFAIHAYKETWF 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 VRLAGGRIPEEGLLEVQVEVNGVPRWGSVCSENWGLTEAMVACRQLGLGFAIHAYKETWF 480
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Qy        481 WSGTPRAQEVVMSGVRCSGTELALQQCQRHGPVHCSHGGGRFLAGVSCMDSAPDLVMNAQ 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 WSGTPRAQEVVMSGVRCSGTELALQQCQRHGPVHCSHGGGRFLAGVSCMDSAPDLVMNAQ 540

Qy        541 LVQETAYLEDRPLSQLYCAHEENCLSKSADHMDWPYGYRRLLRFSTQIYNLGRTDFRPKT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 LVQETAYLEDRPLSQLYCAHEENCLSKSADHMDWPYGYRRLLRFSTQIYNLGRTDFRPKT 600

Qy        601 GRDSWVWHQCHRHYHSIEVFTHYDLLTLNGSKVAEGHKASFCLEDTNCPTGLQRRYACAN 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GRDSWVWHQCHRHYHSIEVFTHYDLLTLNGSKVAEGHKASFCLEDTNCPTGLQRRYACAN 660

Qy        661 FGEQGVTVGCWDTYRHDIDCQWVDITDVGPGNYIFQVIVNPHYEVAESDFSNNMLQCRCK 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 FGEQGVTVGCWDTYRHDIDCQWVDITDVGPGNYIFQVIVNPHYEVAESDFSNNMLQCRCK 720

Qy        721 YDGHRVWLHNCHTGNSYPANAELSLEQEQRLRNNLI 756
              ||||||||||||||||||||||||||||||||||||
Db        721 YDGHRVWLHNCHTGNSYPANAELSLEQEQRLRNNLI 756
```

RESULT 2
AAM48743
ID AAM48743 standard; protein; 756 AA.
XX
AC AAM48743;
XX
DT 02-APR-2002 (first entry)
XX
DE Human 47765 lysyl oxidase SEQ ID NO 2.
XX
KW Human; 47765; lysyl oxidase; LSO; cytostatic; haemostatic; hepatotropic;
KW cardiant; osteopathic; dermatological; antiarteriosclerotic; vasotropic;
KW antiinflammatory; hypotensive; antiarrhythmic; cell proliferation;
KW growth; differentiation; leukaemia; tumour; cancer; bone; cartilage;
KW myeloproliferative; muscular; osteoporosis; cardiovascular; gene therapy;
KW chromosome mapping; tissue typing; forensic; pharmacogenomic; enzyme.
XX
OS Homo sapiens.
XX
PN WO200192495-A2.
XX
PD 06-DEC-2001.
XX
PF 29-MAY-2001; 2001WO-US017405.
XX
PR 26-MAY-2000; 2000US-0207650P.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Meyers R;
XX
DR WPI; 2002-122067/16.
DR N-PSDB; ABA96419, ABA96420.
XX
PT Novel human lysyl oxidase polypeptide, designated 47765, and
PT polynucleotides, useful in the diagnosis and treatment of cell
PT proliferation disorders, muscular disorders, bone disorders and skin
PT elasticity disorders.
XX
PS Claim 14; Fig 1; 115pp; English.
XX
CC The invention relates to human lysyl oxidase (LSO) polypeptide,
CC designated 47765 with cytostatic, haemostatic, hepatotropic, cardiant,
CC osteopathic, dermatological, antiarteriosclerotic, vasotropic,
CC antiinflammatory, hypotensive and antiarrhythmic activity. 47765
CC molecules are useful for identifying a compound which modulates the
CC activity of the protein, for developing novel diagnostic and therapeutic
CC agents for LSO-mediated or related disorders including cell
CC proliferation, growth or differentiation disorder (e.g. carcinoma,
CC leukaemia, tumour angiogenesis, hepatic disorders and haematopoietic,
CC myeloproliferative disorders), muscular disorders (e.g. cardiac muscle
CC disorder, paralysis, ataxia, myotonia and myokymia), bone disorders (e.g.
CC osteochondrosis and osteoporosis), skin elasticity disorders (e.g. cutis
CC laxa, Ehlers-Danlos type V syndrome), cardiovascular disorders (e.g.
CC arteriosclerosis, ischaemia reperfusion injury, restenosis, arterial
CC inflammation, vascular wall remodeling, tachycardia, vascular heart
CC disease, long QT syndrome, congestive heart failure, hypertension,

CC coronary artery disease and arrhythmia) or cartilage based disorders
CC (e.g. chondromalacia and polychondritis). The encoding polynucleotide is
CC useful in chromosome mapping, tissue typing, forensic identification, as
CC markers for pharmacogenomic profiling of a subject and in gene therapy
XX
SQ Sequence 756 AA;

Query Match 99.9%; Score 4174; DB 5; Length 756;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 755; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 MAWSPPATLFLFLLLLGQPPPSRPQSLGTTKLRLVGPESKPEEGRLEVLHQGQWGTVCDD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAWSPPATLFLFLLLLGQPPPSRPQSLGTTKLRLVGPESKPEEGRLEVLHQGQWGTVCDD 60

Qy         61 NFAIQEATVACRQLGFEAALTWAHSAKYGQGEGPIWLDNVRCVGTESSLDQCGSNGWGVS 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 NFAIQEATVACRQLGFEAALTWAHSAKYGQGEGPIWLDNVRCVGTESSLDQCGSNGWGVS 120

Qy        121 DCSHSEDVGVICHPRRHRGYLSETVSNALGPQGRRLEEVRLKPILASAKQHSPVTEGAVE 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 DCSHSEDVGVICHPRRHRGYLSETVSNALGPQGRRLEEVRLKPILASAKQHSPVTEGAVE 180

Qy        181 VKYEGHWRQVCDQGWTMNNSRVVCGMLGFPSEVPVDSHYYRKVWDLKMRDPKSRLKSLTN 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VKYEGHWRQVCDQGWTMNNSRVVCGMLGFPSEVPVDSHYYRKVWDLKMRDPKSRLKSLTN 240

Qy        241 KNSFWIHQVTCLGTEPHMANCQVQVAPARGKLRPACPGGMHAVVSCVAGPHFRPPKTKPQ 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 KNSFWIHQVTCLGTEPHMANCQVQVAPARGKLRPACPGGMHAVVSCVAGPHFRPPKTKPQ 300

Qy        301 RKGSWAEEPRVRLRSGAQVGEGRVEVLMNRQWGTVCDHRWNLISASVVCRQLGFGSAREA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 RKGSWAEEPRVRLRSGAQVGEGRVEVLMNRQWGTVCDHRWNLISASVVCRQLGFGSAREA 360

Qy        361 LFGARLGQGLGPIHLSEVRCRGYERTLSDCPALEGSQNGCQHENAAAVRCNVPNMGFQNQ 420
              |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db        361 LFGARLGQGLGPIHLSEVRCRGYERTLSDCPALEGSQNGCQHENDAAVRCNVPNMGFQNQ 420

Qy        421 VRLAGGRIPEEGLLEVQVEVNGVPRWGSVCSENWGLTEAMVACRQLGLGFAIHAYKETWF 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 VRLAGGRIPEEGLLEVQVEVNGVPRWGSVCSENWGLTEAMVACRQLGLGFAIHAYKETWF 480

Qy        481 WSGTPRAQEVVMSGVRCSGTELALQQCQRHGPVHCSHGGGRFLAGVSCMDSAPDLVMNAQ 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 WSGTPRAQEVVMSGVRCSGTELALQQCQRHGPVHCSHGGGRFLAGVSCMDSAPDLVMNAQ 540

Qy        541 LVQETAYLEDRPLSQLYCAHEENCLSKSADHMDWPYGYRRLLRFSTQIYNLGRTDFRPKT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 LVQETAYLEDRPLSQLYCAHEENCLSKSADHMDWPYGYRRLLRFSTQIYNLGRTDFRPKT 600

Qy        601 GRDSWVWHQCHRHYHSIEVFTHYDLLTLNGSKVAEGHKASFCLEDTNCPTGLQRRYACAN 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GRDSWVWHQCHRHYHSIEVFTHYDLLTLNGSKVAEGHKASFCLEDTNCPTGLQRRYACAN 660

Qy        661 FGEQGVTVGCWDTYRHDIDCQWVDITDVGPGNYIFQVIVNPHYEVAESDFSNNMLQCRCK 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        661 FGEQGVTVGCWDTYRHDIDCQWVDITDVGPGNYIFQVIVNPHYEVAESDFSNNMLQCRCK 720

Qy        721 YDGHRVWLHNCHTGNSYPANAELSLEQEQRLRNNLI 756
              |||||||||||||||||||||||||||||||||||||
Db        721 YDGHRVWLHNCHTGNSYPANAELSLEQEQRLRNNLI 756
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US-09-924-946-2
; Sequence 2, Application US/09924946
; Patent No. US20020102645A1
; GENERAL INFORMATION:
; APPLICANT: American Home Products Corporation
; APPLICANT: Evans, Mark
; APPLICANT: Scicchitano, Marshall
; APPLICANT: Bapat, Ashok
; APPLICANT: Beer, Eric
; APPLICANT: Bhat, Ramesh
; APPLICANT: Ferris, Elissa
; APPLICANT: Mastroeni, Rob
; APPLICANT: Zhang, Jianxiong
; APPLICANT: Karathanasis, Sotirios K.
; TITLE OF INVENTION: A No. US20020102645A1el Member of the Lysyl Oxidase Gene Family
; FILE REFERENCE: 0630/1G703-US2
; CURRENT APPLICATION NUMBER: US/09/924,946
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/223,763
; PRIOR FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: 60/255,838
; PRIOR FILING DATE: 2000-12-15
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 756
; TYPE: PRT
; ORGANISM: Human
US-09-924-946-2

Query Match 100.0%; Score 103; DB 9; Length 756;
Best Local Similarity 100.0%; Pred. No. 4.4e-99;
Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 LRLVGPESKPEEGRLEVLHQGQWGTVCDDNFAIQEATVACRQLGFEAALTWAHSAKYGQG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         32 LRLVGPESKPEEGRLEVLHQGQWGTVCDDNFAIQEATVACRQLGFEAALTWAHSAKYGQG 91

Qy         61 EGPIWLDNVRCVGTESSLDQCGSNGWGVSDCSHSEDVGVICHP 103
              |||||||||||||||||||||||||||||||||||||||||||
Db         92 EGPIWLDNVRCVGTESSLDQCGSNGWGVSDCSHSEDVGVICHP 134
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RESULT 6
US-09-924-946-2
; Sequence 2, Application US/09924946
; Patent No. US20020102645A1
; GENERAL INFORMATION:
; APPLICANT: American Home Products Corporation
; APPLICANT: Evans, Mark
; APPLICANT: Scicchitano, Marshall
; APPLICANT: Bapat, Ashok
; APPLICANT: Beer, Eric
; APPLICANT: Bhat, Ramesh
; APPLICANT: Ferris, Elissa
; APPLICANT: Mastroeni, Rob
; APPLICANT: Zhang, Jianxiong
; APPLICANT: Karathanasis, Sotirios K.
; TITLE OF INVENTION: A No. US20020102645A1el Member of the Lysyl Oxidase Gene Family
; FILE REFERENCE: 0630/1G703-US2
; CURRENT APPLICATION NUMBER: US/09/924,946
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/223,763
; PRIOR FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: 60/255,838
; PRIOR FILING DATE: 2000-12-15
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 756
; TYPE: PRT
; ORGANISM: Human
US-09-924-946-2

Query Match 100.0%; Score 125; DB 9; Length 756;
Best Local Similarity 100.0%; Pred. No. 1.2e-121;
Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 PILASAKQHSPVTEGAVEVKYEGHWRQVCDQGWTMNNSRVVCGMLGFPSEVPVDSHYYRK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        163 PILASAKQHSPVTEGAVEVKYEGHWRQVCDQGWTMNNSRVVCGMLGFPSEVPVDSHYYRK 222

Qy         61 VWDLKMRDPKSRLKSLTNKNSFWIHQVTCLGTEPHMANCQVQVAPARGKLRPACPGGMHA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        223 VWDLKMRDPKSRLKSLTNKNSFWIHQVTCLGTEPHMANCQVQVAPARGKLRPACPGGMHA 282

Qy        121 VVSCV 125
              |||||
Db        283 VVSCV 287
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RESULT 3
US-09-924-946-2
; Sequence 2, Application US/09924946
; Patent No. US20020102645A1
; GENERAL INFORMATION:
; APPLICANT: American Home Products Corporation
; APPLICANT: Evans, Mark
; APPLICANT: Scicchitano, Marshall
; APPLICANT: Bapat, Ashok
; APPLICANT: Beer, Eric
; APPLICANT: Bhat, Ramesh
; APPLICANT: Ferris, Elissa
; APPLICANT: Mastroeni, Rob
; APPLICANT: Zhang, Jianxiong
; APPLICANT: Karathanasis, Sotirios K.
; TITLE OF INVENTION: A No. US20020102645A1el Member of the Lysyl Oxidase Gene Family
; FILE REFERENCE: 0630/1G703-US2
; CURRENT APPLICATION NUMBER: US/09/924,946
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/223,763
; PRIOR FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: 60/255,838
; PRIOR FILING DATE: 2000-12-15
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 756
; TYPE: PRT
; ORGANISM: Human
US-09-924-946-2

Query Match 100.0%; Score 101; DB 9; Length 756;
Best Local Similarity 100.0%; Pred. No. 2.5e-90;
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 VRLRSGAQVGEGRVEVLMNRQWGTVCDHRWNLISASVVCRQLGFGSAREALFGARLGQGL 60
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Db        311 VRLRSGAQVGEGRVEVLMNRQWGTVCDHRWNLISASVVCRQLGFGSAREALFGARLGQGL 370

Qy         61 GPIHLSEVRCRGYERTLSDCPALEGSQNGCQHENAAAVRCN 101
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Db        371 GPIHLSEVRCRGYERTLSDCPALEGSQNGCQHENAAAVRCN 411
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RESULT 6
US-09-924-946-2
; Sequence 2, Application US/09924946
; Patent No. US20020102645A1
; GENERAL INFORMATION:
; APPLICANT: American Home Products Corporation
; APPLICANT: Evans, Mark
; APPLICANT: Scicchitano, Marshall
; APPLICANT: Bapat, Ashok
; APPLICANT: Beer, Eric
; APPLICANT: Bhat, Ramesh
; APPLICANT: Ferris, Elissa
; APPLICANT: Mastroeni, Rob
; APPLICANT: Zhang, Jianxiong
; APPLICANT: Karathanasis, Sotirios K.
; TITLE OF INVENTION: A No. US20020102645A1el Member of the Lysyl Oxidase Gene Family
; FILE REFERENCE: 0630/1G703-US2
; CURRENT APPLICATION NUMBER: US/09/924,946
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/223,763
; PRIOR FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: 60/255,838
; PRIOR FILING DATE: 2000-12-15
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 756
; TYPE: PRT
; ORGANISM: Human
US-09-924-946-2

Query Match 100.0%; Score 109; DB 9; Length 756;
Best Local Similarity 100.0%; Pred. No. 5.8e-99;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         61 WSGTPRAQEVVMSGVRCSGTELALQQCQRHGPVHCSHGGGRFLAGVSCM 109
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RESULT 4
US-09-924-946-2
; Sequence 2, Application US/09924946
; Patent No. US20020102645A1
; GENERAL INFORMATION:
; APPLICANT: American Home Products Corporation
; APPLICANT: Evans, Mark
; APPLICANT: Scicchitano, Marshall
; APPLICANT: Bapat, Ashok
; APPLICANT: Beer, Eric
; APPLICANT: Bhat, Ramesh
; APPLICANT: Ferris, Elissa
; APPLICANT: Mastroeni, Rob
; APPLICANT: Zhang, Jianxiong
; APPLICANT: Karathanasis, Sotirios K.
; TITLE OF INVENTION: A No. US20020102645A1el Member of the Lysyl Oxidase Gene Family
; FILE REFERENCE: 0630/1G703-US2
; CURRENT APPLICATION NUMBER: US/09/924,946
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/223,763
; PRIOR FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: 60/255,838
; PRIOR FILING DATE: 2000-12-15
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 756
; TYPE: PRT
; ORGANISM: Human
US-09-924-946-2

Query Match 100.0%; Score 227; DB 9; Length 756;
Best Local Similarity 100.0%; Pred. No. 2.1e-223;
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         61 NLGRTDFRPKTGRDSWVWHQCHRHYHSIEVFTHYDLLTLNGSKVAEGHKASFCLEDTNCP 120
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Db        590 NLGRTDFRPKTGRDSWVWHQCHRHYHSIEVFTHYDLLTLNGSKVAEGHKASFCLEDTNCP 649

Qy        121 TGLQRRYACANFGEQGVTVGCWDTYRHDIDCQWVDITDVGPGNYIFQVIVNPHYEVAESD 180
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Db        650 TGLQRRYACANFGEQGVTVGCWDTYRHDIDCQWVDITDVGPGNYIFQVIVNPHYEVAESD 709

Qy        181 FSNNMLQCRCKYDGHRVWLHNCHTGNSYPANAELSLEQEQRLRNNLI 227
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RESULT 4
AX323479
LOCUS AX323479 2976 bp DNA linear PAT 07-JAN-2002
DEFINITION Sequence 1 from Patent WO0192495.
ACCESSION AX323479
VERSION AX323479.1 GI:18094234
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Meyers,R.
TITLE A human lysyl oxidase (47765) and uses thereof
JOURNAL Patent: WO 0192495-A 1 06-DEC-2001;
Millennium Pharmaceuticals, Inc. (US)
FEATURES Location/Qualifiers
source 1. .2976
/organism="Homo sapiens"
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/db_xref="taxon:9606"
CDS 95. .2365
/note="unnamed protein product"
/codon_start=1
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/db_xref="GI:18094235"
/db_xref="REMTREMBL:CAD20417"
/translation="MAWSPPATLFLFLLLLGQPPPSRPQSLGTTKLRLVGPESKPEEG
RLEVLHQGQWGTVCDDNFAIQEATVACRQLGFEAALTWAHSAKYGQGEGPIWLDNVRC
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LKPILASAKQHSPVTEGAVEVKYEGHWRQVCDQGWTMNNSRVVCGMLGFPSEVPVDSH
YYRKVWDLKMRDPKSRLKSLTNKNSFWIHQVTCLGTEPHMANCQVQVAPARGKLRPAC
PGGMHAVVSCVAGPHFRPPKTKPQRKGSWAEEPRVRLRSGAQVGEGRVEVLMNRQWGT
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LLTLNGSKVAEGHKASFCLEDTNCPTGLQRRYACANFGEQGVTVGCWDTYRHDIDCQW
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ORIGIN

Query Match 78.7%; Score 2844.4; DB 6; Length 2976;
Best Local Similarity 97.6%; Pred. No. 0;
Matches 2872; Conservative 11; Mismatches 59; Indels 0; Gaps 0;

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Qy          60 CAAGCCCCCTCTTTCCTAGCCTGGACAGGTATCTTGGCCTCAGCTGTCCTTGAAGTCACC 119
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Db          35 CAGCCCCGGACTGTCCGCGCTCCATCTGGTATCTTGGCCTCAGCTGTCCTTGAAGTCACC 94

Qy         120 ATGGCGTGGTCCCCACCAGCCACCCTCTTTCTGTTCCTGCTGCTGCTAGGCCAGCCCCCT 179
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Db          95 ATGGCGTGGTCCCCACCAGCCACCCTCTTTCTGTTCCTGCTGCTGCTAGGCCAGCCCCCT 154

Qy         180 CCCAGCAGGCCACAGTCACTGGGCACCACTAAGCTCCGGCTGGTGGGCCCAGAGAGCAAG 239
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Qy        240 CCAGAGGAGGGCCGCCTGGAGGTGCTGCACCAGGGCCAGTGGGGCACCGTGTGTGATGAC 299
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Qy        300 AACTTTGCTATCCAGGAGGCCACAGTGGCTTGCCGCCAGCTGGGCTTCGAAGCTGCCTTG 359
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Qy        360 ACCTGGGCCCACAGTGCCAAGTACGGCCAAGGGGAGGGACCCATCTGGCTGGACAATGTG 419
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Db        335 ACCTGGGCCCACAGTGCCAAGTACGGCCAAGGGGAGGGACCCATCTGGCTGGACAATGTG 394

Qy        420 CGCTGTGTGGGCACAGAGAGCTCCTTGGACCAGTGCGGGTCTAATGGCTGGGGAGTCAGT 479
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        395 CGCTGTGTGGGCACAGAGAGCTCCTTGGACCAGTGCGGGTCTAATGGCTGGGGAGTCAGT 454

Qy        480 GACTGCAGTCACTCAGAAGACGTAGGGGTGATATGCCACCCCCGGCGCCATCGTGGCTAC 539
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Db        455 GACTGCAGTCACTCAGAAGACGTAGGGGTGATATGCCACCCCCGGCGCCATCGTGGCTAC 514

Qy        540 CTTTCTGAAACTGTCTCCAATGCCCTTGGGCCCCAGGGCCGGCGGCTGGAGGAGGTGCGG 599
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Qy        600 CTCAAGCCCATCCTTGCCAGTGCCAAGCAGCATAGCCCAGTGACCGAGGGAGCCGTGGAG 659
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Db        575 CTCAAGCCCATCCTTGCCAGTGCCAAGCAGCATAGCCCAGTGACCGAGGGAGCCGTGGAG 634

Qy        660 GTGAAGTATGAGGGCCACTGGCGGCAGGTGTGTGACCAGGGCTGGACCATGAACAACAGC 719
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Db        635 GTGAAGTATGAGGGCCACTGGCGGCAGGTGTGTGACCAGGGCTGGACCATGAACAACAGC 694

Qy        720 AGGGTGGTGTGCGGGATGCTGGGCTTCCCCAGCGAGGTGCCTGTCGACAGCCACTACTAC 779
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Qy        780 AGGAAAGTCTGGGATCTGAAGATGAGGGACCCTAAGTCTAGGCTGAAGAGCCTGACGAAT 839
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Db        755 AGGAAAGTCTGGGATCTGAAGATGAGGGACCCTAAGTCTAGGCTGAAGAGCCTGACGAAT 814

Qy        840 AAGAACTCCTTCTGGATCCACCAGGTCACCTGCCTGGGGACAGAGCCCCACATGGCCAAC 899
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Qy        900 TGCCAGGTGCAGGTGGCTCCAGCCCGGGGCAAGCTGCGGCCAGCCTGCCCAGGTGGCATG 959
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Qy       1020 CGCAAAGGGTCCTGGGCAGAGGAGCCGAGGGTGCGCCTGCGCTCCGGGGCCCAGGTGGGC 1079
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Qy       1080 GAGGGCCGGGTGGAAGTGCTCATGAACCGCCAGTGGGGCACGGTCTGTGACCACAGGTGG 1139
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Db       1055 GAGGGCCGGGTGGAAGTGCTCATGAACCGCCAGTGGGGCACGGTCTGTGACCACAGGTGG 1114

Qy       1140 AACCTCATCTCTGCCAGTGTCGTGTGTCGTCAGCTGGGCTTTGGCTCTGCTCGGGAGGCC 1199
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Qy       1260 AGGGGATATGAGCGGACCCTCAGCGACTGCCCTGCCCTGGAAGGGTCCCAGAATGGTTGC 1319
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Qy       1380 GTGCGCTTGGCTGGTGGGCGTATCCCTGAGGAGGGGCTATTGGAGGTGCAGGTGGAGGTG 1439
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Qy       1440 AACGGGGTCCCACGCTGGGGGAGCGTGTGCAGTGAAAACTGGGGGCTCACCGAAGCCATG 1499
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Qy       1560 TGGTCGGGGACGCCAAGGGCCCAGGAGGTGGTGATGAGTGGGGTGCGCTGCTCAGGCACA 1619
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Qy       1680 CGCTTCCTGGCTGGAGTCTCCTGCATGGACAGTGCACCAGACCTGGTGATGAACGCCCAG 1739
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Qy       1740 CTAGTGCAGGAGACGGCCTACTTGGAGGACCGCCCGCTCAGCCAGCTGTATTGTGCCCAC 1799
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Qy       1800 GAGGAGAACTGCCTCTCCAAGTCTGCGGATCACATGGACTGGCCCTACGGATACCGCCGC 1859
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Db       1775 GAGGAGAACTGCCTCTCCAAGTCTGCAGATCACATGGACTGGCCCTACGGATACCGCCGC 1834

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Db       1835 CTATTGCGCTTCTCCACACAGATCTACAATCTGGGCCGGACTGACTTTCGTCCAAAGACT 1894
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Qy       1920 GGACGCGATAGCTGGGTTTGGCACCAGTGCCACAGGCATTACCACAGCATTGAGGTCTTC 1979
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Db       1895 GGACGCGATAGCTGGGTTTGGCACCAGTGCCACAGGCATTACCACAGCATTGAGGTCTTC 1954

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Qy       2040 TTCTGTCTGGAGGACACAAACTGCCCCACAGGACTGCAGCGGCGCTACGCATGTGCCAAC 2099
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Qy       2100 TTTGGAGAACAGGGAGTGACTGTAGGCTGCTGGGACACCTACCGGCATGACATTGATTGC 2159
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Db       2615 CTCCTCTTCTGTAAGGAAACCCAGTCATCCCTGAATCTTGCCACAGAGATCCGGGATTCA 2674

Qy       2700 GGAGCTCTCAGTTTCTTAGGGATGGACTATGGCCCAGTCCCCCATCTAAGTGGTGCTTTG 2759
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||:||||||
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Qy       2940 TAGTGTCCTTACCTTTATCTTACCACACACATGGGTGTTTCTATTATCCTTGGAAGCACA 2999
                ||| | |||||:|||||| |::|   : : || || | || |||||||:||||||||||||
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Qy       3000 GA 3001
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Db       2975 AA 2976
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